

FIG.1A

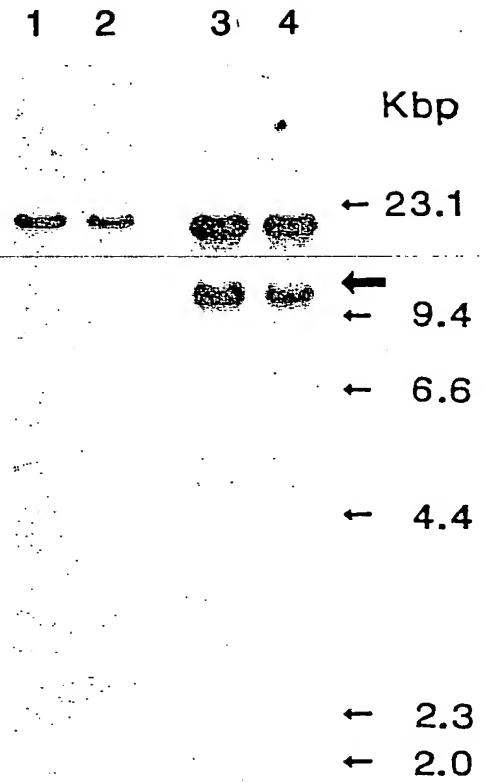


FIG.1B

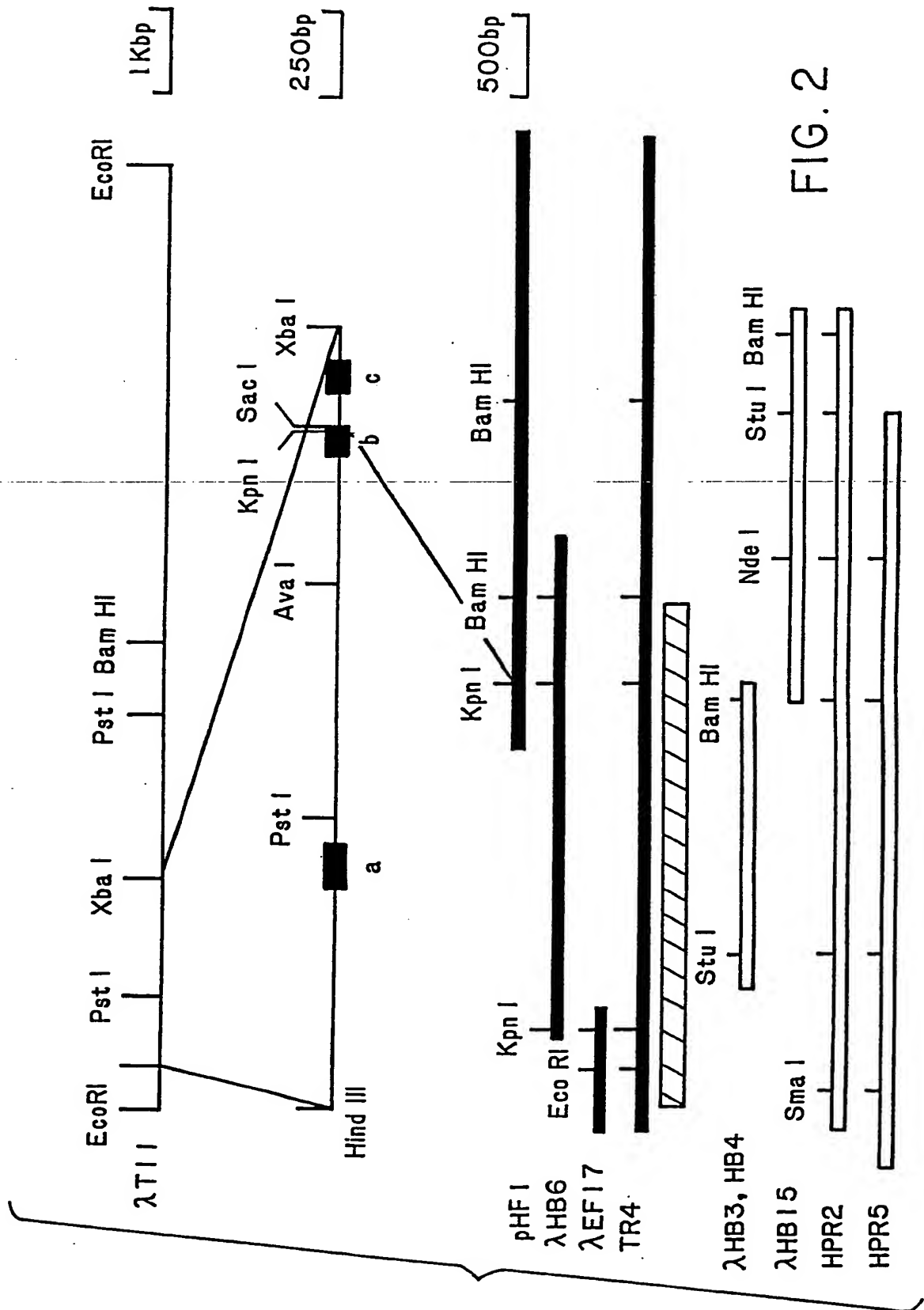


FIG. 2

FIG. 3-1

1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGA

49 TCATTTGGGAAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATT

100 CATTGCGGAATAACATCGGAGGAGAAGTTTCCCAGAGCTATGGGG MetGly

5 10 15

ThrSerHisProAlaPheLeuValLeuGlyCysLeuLeuThrGly

145 ACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGG

20 25 30

LeuSerLeuIleLeuCysGlnLeuSerLeuProSerIleLeuPro

190 CTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCA

35 40 45

AsnGluAsnGluLysValValGlnLeuAsnSerSerPheSerLeu

235 AATGAAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTG

50 55 60

ArgCysPheGlyGluSerGluValSerTrpGlnTyrProMetSer

280 AGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCCATGTCT

65 70 75

GluGluGluSerSerAspValGluIleArgAsnGluGluAsnAsn

325 GAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAAC

80 85 90

SerGlyLeuPheValThrValLeuGluValSerSerAlaSerAla

370 AGCGGCCTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCG

95 100 105

AlaHisThrGlyLeuTyrThrCysTyrTyrAsnHisThrGlnThr

415 GCCCACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACA

110 115 120

GluGluAsnGluLeuGluGlyArgHisIleTyrIleTyrValPro

460 GAAGAGAAATGAGCTTGAAGGCAGGCACATTTACATCTATGTGCCA

125 130 135

AspProAspValAlaPheValProLeuGlyMetThrAspTyrLeu

505 GACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTA

FIG. 3-2

```

140          145          150
ValIleValGluAspAspAspSerAlaIleIleProCysArgThr
550 GTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACA

155          160          165
ThrAspProGluThrProValThrLeuHisAsnSerGluGlyVal
595 ACTGATCCCGAGACTCCTGTAACTTACACAACAGTGAGGGGGTG

170          175          180
ValProAlaSerTyrAspSerArgGlnGlyPheAsnGlyThrPhe
640 GTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGGACCTTC

185          190          195
ThrValGlyProTyrIleCysGluAlaThrValLysGlyLysLys
685 ACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAG

200          205          210
PheGlnThrIleProPheAsnValTyrAlaLeuLysAlaThrSer
730 TTCCAGACCATCCCATTTAATGTTTATGCTTTAAAGCAACATCA

215          220          225
GluLeuAspLeuGluMetGluAlaLeuLysThrValTyrLysSer
775 GAGCTGGATCTAGAAATGGAAGCTCTTAAACCGTGATAAGTCA

230          235          240
GlyGluThrIleValValThrCysAlaValPheAsnAsnGluVal
820 GGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAATGAGGTG

245          250          255
ValAspLeuGlnTrpThrTyrProGlyGluValLysGlyLysGly
865 GTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGC

260          265          270
IleThrMetLeuGluGluIleLysValProSerIleLysLeuVal
910 ATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTG

275          280          285
TyrThrLeuThrValProGluAlaThrValLysAspSerGlyAsp
955 TACACTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGAGAT

290          295          300
TyrGluCysAlaAlaArgGlnAlaThrArgGluValLysGluMet
1000 TACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAAGAAATG

305          310          315
LysLysValThrIleSerValHisGluLysGlyPheIleGluIle
1045 AAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATC

```

FIG. 3-3

```

      320              325              330
LysProThrPheSerGlnLeuGluAlaValAsnLeuHisGluVal
1090 AAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTC

      335              340              345
LysHisPheValValGluValArgAlaTyrProProProArgIle
1135 AAACATTTTGTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATA

      350              355              360
SerTrpLeuLysAsnAsnLeuThrLeuIleGluAsnLeuThrGlu
1180 TCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTCACTGAG

      365              370              375
IleThrThrAspValGluLysIleGlnGluIleArgTyrArgSer
1225 ATCACCCTGATGTGGAAAAGATTGAGGAAATAAGGTATCGAAGC

      380              385              390
LysLeuLysLeuIleArgAlaLysGluGluAspSerGlyHisTyr
1270 AAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTAT

      395              400              405
ThrIleValAlaGlnAsnGluAspAlaValLysSerTyrThrPhe
1315 ACTATTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTT

      410              415              420
GluLeuLeuThrGlnValProSerSerIleLeuAspLeuValAsp
1360 GAACTGTAACTCAAGTTCCTTCATCCATTCTGGACTTGGTCGAT

      425              430              435
AspHisHisGlySerThrGlyGlyGlnThrValArgCysThrAla
1405 GATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCT

      440              445              450
GluGlyThrProLeuProAspIleGluTrpMetIleCysLysAsp
1450 GAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGAT

      455              460              465
IleLysLysCysAsnAsnGluThrSerTrpThrIleLeuAlaAsn
1495 ATTAAGAAATGTAATAATGAACTTCCTGGACTATTTTGGCCAAC

      470              475              480
AsnValSerAsnIleIleThrGluIleHisSerArgAspArgSer
1540 AATGTCTCAAACATCATCACGGAGATCCACTCCCGAGACAGGAGT

      485              490              495
ThrValGluGlyArgValThrPheAlaLysValGluGluThrIle
1585 ACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATC

```

FIG. 3-4

```

      500      505      510
AlaValArgCysLeuAlaLysAsnLeuLeuGlyAlaGluAsnArg
1630 GCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGA

      515      520      525
GluLeuLysLeuValAlaProThrLeuArgSerGluLeuThrVal
1675 GAGCTGAAGCTGGTGGCTCCACCCCTGCGTTCTGAACTCACGGTG

      530      535      540
AlaAlaAlaValLeuValLeuValIleValIleIleSerLeu
1720 GCTGCTGCAGTCCTGGTGTGTTGGTGATTGTGATCATCTCACTT

      545      550      555
IleValLeuValValIleTrpLysGlnLysProArgTyrGluIle
1765 ATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATT

-----
      560      565      570
ArgTrpArgValIleGluSerIleSerProAspGlyHisGluTyr
1810 CGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATAT

      575      580      585
IleTyrValAspProMetGlnLeuProTyrAspSerArgTrpGlu
1855 ATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAG

      590      595      600
PheProArgAspGlyLeuValLeuGlyArgValLeuGlySerGly
1900 TTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGA

      605      610      615
AlaPheGlyLysValValGluGlyThrAlaTyrGlyLeuSerArg
1945 GCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGG

      620      625      630
SerGlnProValMetLysValAlaValLysMetLeuLysProThr
1990 TCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACG

      635      640      645
AlaArgSerSerGluLysGlnAlaLeuMetSerGluLeuLysIle
2035 GCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATA

      650      655      660
MetThrHisLeuGlyProHisLeuAsnIleValAsnLeuLeuGly
2080 ATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGA

      665      670      675
AlaCysThrLysSerGlyProIleTyrIleIleThrGluTyrCys
2125 GCCTGCACCAAGTCAGGCCCATTTACATCATCACAGAGTATTGC

```

FIG. 3-5

	680	685	690
	PheTyrGlyAspLeuValAsnTyrLeuHisLysAsnArgAspSer		
2170	TTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGC		
	695	700	705
	PheLeuSerHisHisProGluLysProLysLysGluLeuAspIle		
2215	TTCCTGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATC		
	710	715	720
	PheGlyLeuAsnProAlaAspGluSerThrArgSerTyrValIle		
2260	TTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATT		
	725	730	735
	LeuSerPheGluAsnAsnGlyAspTyrMetAspMetLysGlnAla		
2305	TTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCT		
	740	745	750
	AspThrThrGlnTyrValProMetLeuGluArgLysGluValSer		
2350	GATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCT		
	755	760	765
	LysTyrSerAspIleGlnArgSerLeuTyrAspArgProAlaSer		
2395	AAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCA		
	770	775	780
	TyrLysLysLysSerMetLeuAspSerGluValLysAsnLeuLeu		
2440	TATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTT		
	785	790	795
	SerAspAspAsnSerGluGlyLeuThrLeuLeuAspLeuLeuSer		
2485	TCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGC		
	800	805	810
	PheThrTyrGlnValAlaArgGlyMetGluPheLeuAlaSerLys		
2530	TTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAA		
	815	820	825
	Asn <u>Cys</u> ValHisArgAspLeuAlaAlaArgAsnValLeuLeuAla		
2575	AATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCA		
	830	835	840
	GlnGlyLysIleValLysIleCysAspPheGlyLeuAlaArgAsp		
2620	CAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGAC		
	845	850	855
	IleMetHisAspSerAsnTyrValSerLysGlySerThrPheLeu		
2665	ATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTG		

FIG. 3-6

860 865 870
ProValLysTrpMetAlaProGluSerIlePheAspAsnLeuTyr
2710 CCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTAC
a

875 880 885
ThrThrLeuSerAspValTrpSerTyrGlyIleLeuLeuTrpGlu
2755 ACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAG

890 895 900
IlePheSerLeuGlyGlyThrProTyrProGlyMetMetValAsp
2800 ATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGAT
/\

905 910 915
SerThrPheTyrAsnLysIleLysSerGlyTyrArgMetAlaLys
2845 TCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAG
b

920 925 930
ProAspHisAlaThrSerGluValTyrGluIleMetValLysCys
2890 CCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGC
/\

935 940 945
TrpAsnSerGluProGluLysArgProSerPheTyrHisLeuSer
2935 TGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGT
c

950 955 960
GluIleValGluAsnLeuLeuProGlyGlnTyrLysLysSerTyr
2980 GAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTAT
/

965 970 975
GluLysIleHisLeuAspPheLeuLysSerAspHisProAlaVal
3025 GAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTG

980 985 990
AlaArgMetArgValAspSerAspAsnAlaTyrIleGlyValThr
3070 GCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCAAC

995 1000 1005
TyrLysAsnGluGluAspLysLeuLysAspTrpGluGlyGlyLeu
3115 TACAAAAACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTG

FIG. 3-7

1010	1015	1020
AspGluGlnArgLeuSerAlaAspSerGlyTyrIleIleProLeu		
3160 GATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTCTG		
1025	1030	1035
ProAspIleAspProValProGluGluGluAspLeuGlyLysArg		
3205 CCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGG		
1040	1045	1050
AsnArgHisSerSerGlnThrSerGluGluSerAlaIleGluThr		
3250 AACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACG		
1055	1060	1065
GlySerSerSerSerThrPheIleLysArgGluAspGluThrIle		
3295 GGTTCCAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATT		
1070	1075	1080
GluAspIleAspMetMetAspAspIleGlyIleAspSerSerAsp		
3340 GAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAGAC		
1085		
LeuValGluAspSerPheLeu		
3385 CTGGTGGAAGACAGCTTCCTGTAAGTGGCGGATTCGAGGGGTTCC		
3430 TTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTT		
3475 TATTGCAATGCGGAGGTTGAGAGGAGGACTTGTTGATGTTTAAA		
3520 GAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAAATATGAA		
3565 TGAATGGGATATTTTGAATGAACTTTGTCAGTGTTGCCTCTCGC		
3610 AATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGA		
3655 TGGATAAGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCA		
3700 AGGACATTGGTGAGAGTCCAACAGACACAATTTATACTGCGACAG		
3745 AACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTG		
3790 TTTAGATTGTATTAATACTATCTTCTTTGGACTTCTGAAGAGACCAC		
3835 TCAATCCATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGC		
3880 TGTTGAACTTTTTTAAAGAAGTGCATGAAAAACCATTTTTTGAACCT		
3925 TAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTT		

FIG. 3-8

3970 AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTG
4015 GGTCATTTAGAAAGCCTGACAACTCATTTTCATATTGTAATCTATG
4060 TTTATAATACTACTACTGTTATCAGTAATGCTAAATGTGTAATAA
4105 TGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCC
4150 TTAATAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTA
4195 AATAACATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATT
4240 AAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGTGTTGTCCA
4285 GGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCAT

4330 CGTATTAAAAACAATTAAGTCCCTCTGAAATAATGGGATTAGA
4375 AACAAACAAAACCTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCA
4420 TAAACCTGTGCTGAACATAACTTCTCATGTATATTACCCAATGGA
4465 AAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTT
4510 TTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATAT
4555 GTATTTTTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCC
4600 AGACATCAGCCTCCTTCTTTACCCCTTACCCCAAAGAGAAAGAG
4645 TTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGAT
4690 GTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCA
4735 GGATGACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATG
4780 AAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAACTCCCTGGC
4825 TGTTCTGATCGGCCAGTTTTTCGGAAACACTGACTTAGGTTTCAGG
4870 AAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTG
4915 GAATTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCA
4960 GGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAA
5005 TTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGG

FIG. 3-9

5050 TTTTGACAGGTTTTCCTAAAGATGCTACTTCCCACTGTAT
5095 GGGGGAGATTGAACTTTCCTCGTCTCCCGTCTTCTGCCTCCCACT
5140 CCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCA
5185 GTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGA
5230 AACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATG
5275 AATTGTCACATCTATCCCACTGTCAAACAGGTTGGTGTGGGTTC
5320 ATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAA
5365 TGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGA
5410 TGATGCTTTGGAAGATGCAGAAGCAATAATAAGTACTTGACTAC
5455 CTACTGGTGTAACTCTCAATGCAAGCCCCAACTTTCTTATCCA
5500 TTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAA
5545 ACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATA
5590 CGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCT
5635 CACTCTCCCTTGACAGCCTTATTTTGTGTTGGTGCTTTGCATTTTG
5680 ATATTGCTGTGAGCCTTGACATGACATCATGAGGCCGGATGAACT
5725 TCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAA
5770 TTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTTCAGCAA
5815 TTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGA
5860 AAATTTGCCAATCTTTCCTACTTTCTATTTTATGATGACAATCA
5905 AAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGT
5950 GATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTA
5995 TTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAAT
6040 ATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAA
6085 CATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAA

Inventor:
Title:
Serial No.
Docket No.
Sheet:

Matsui, T.
Antibodies for the Alpha Platelet-
Derived Growth Factor Receptor
Unassigned
14014.00266U3
12 of 27

6130 CTGTGATAATCCCCACAGGCACATTAAGTGTGCACTTTTGAATG
6175 TCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACA

6220 TGTTCCTCCAAAACAATGGTGTGGTGAATGTGTGAGAAAACTAACT
6265 TGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCCTGTTC
6310 ATGTTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAA
6355 TAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAAAAAA
6400 AAAAAAAAAAAAAA

FIG. 3-10

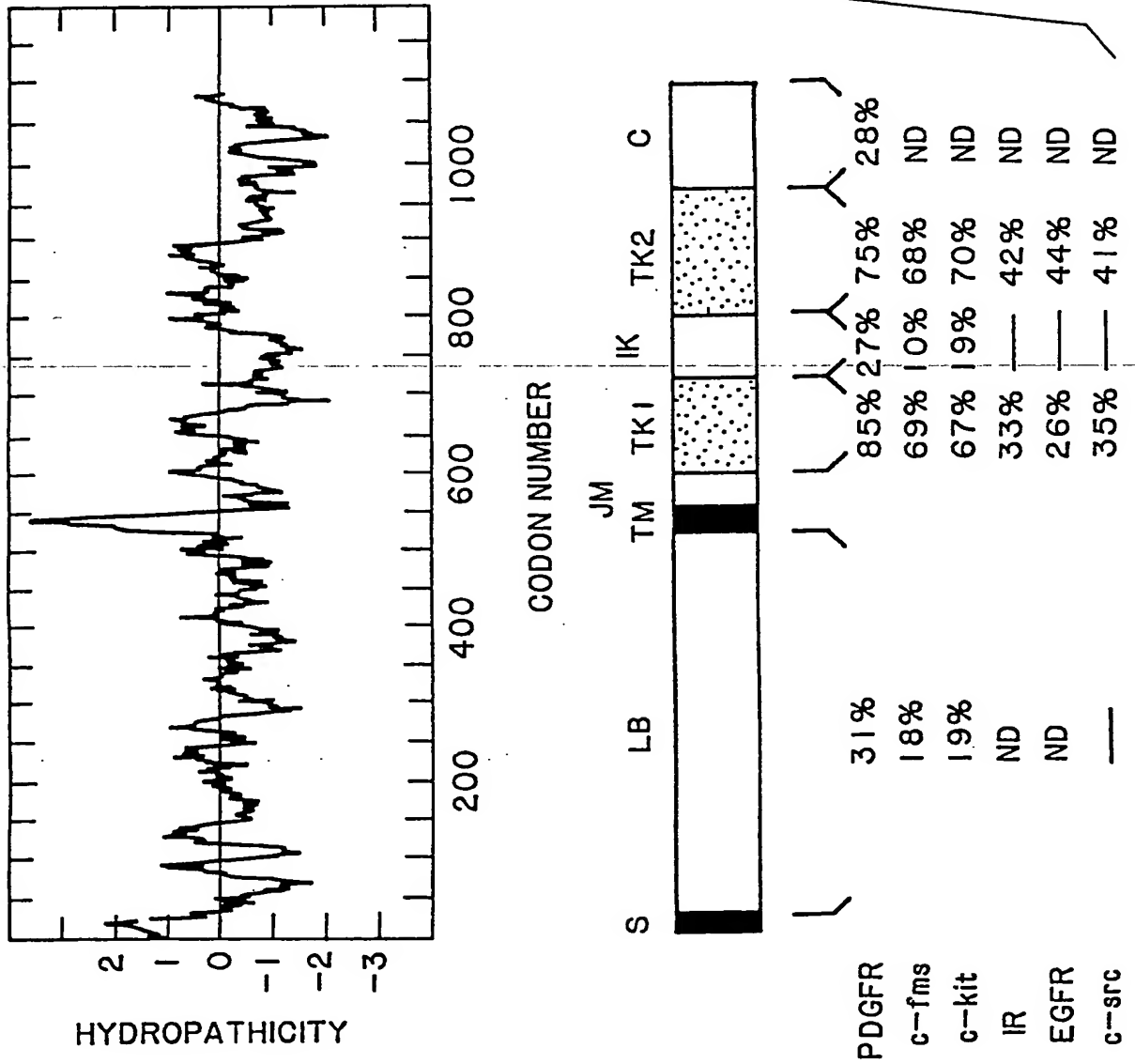
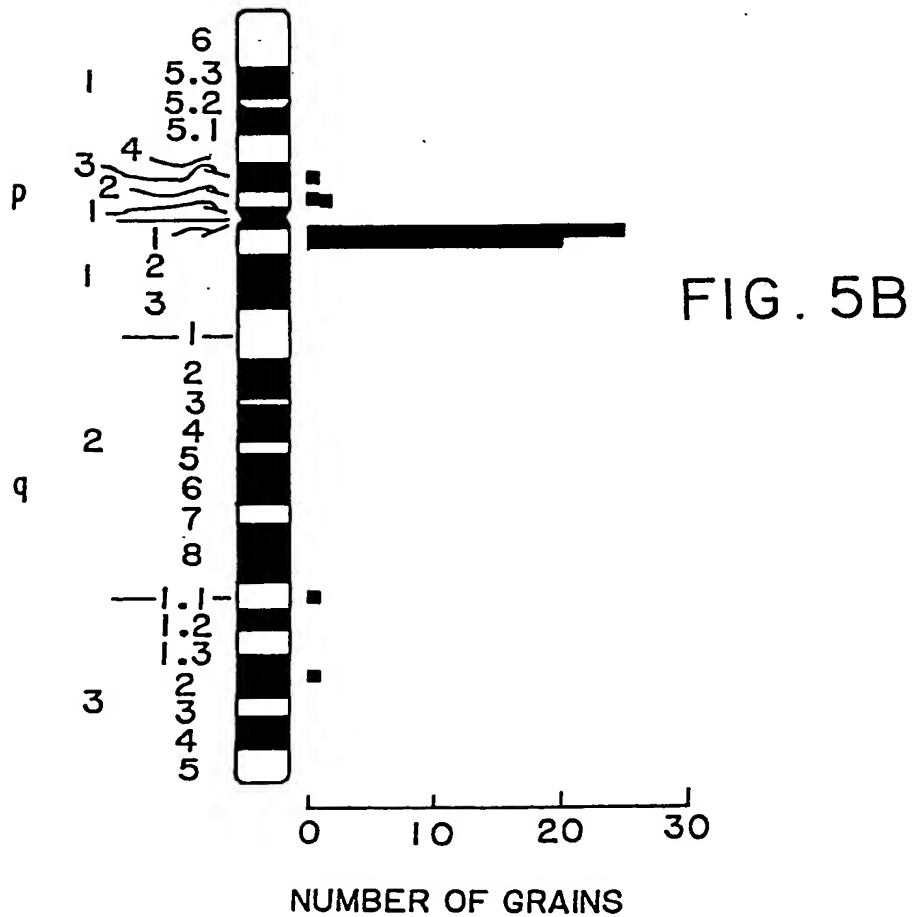
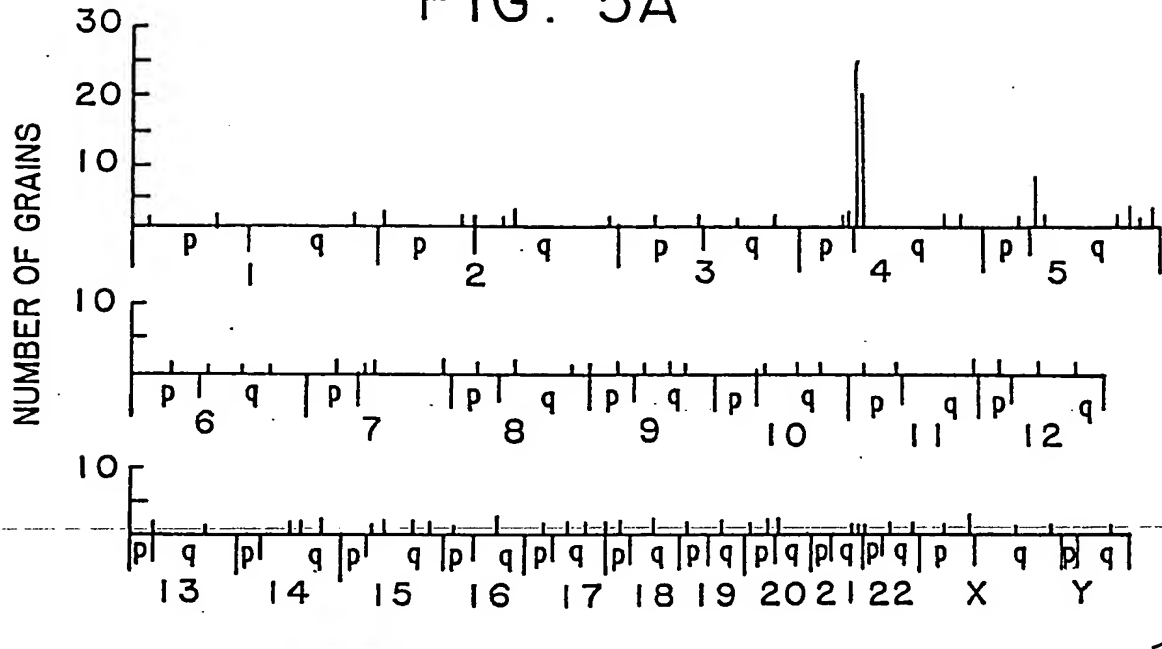


FIG. 4

FIG. 5A



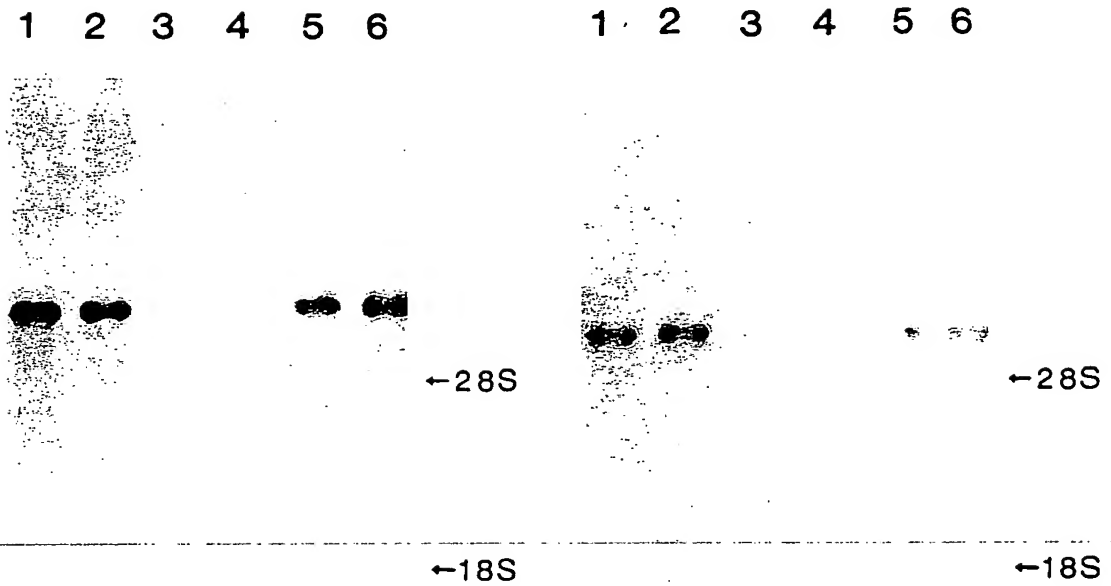


FIG. 6A

FIG. 6B



FIG. 6C

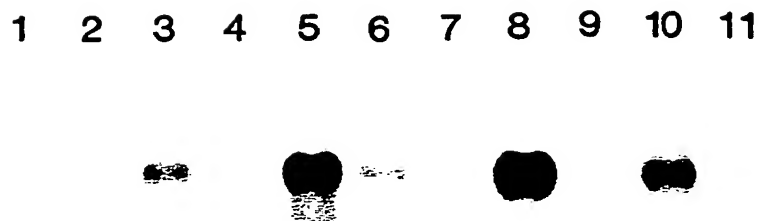


FIG. 6D

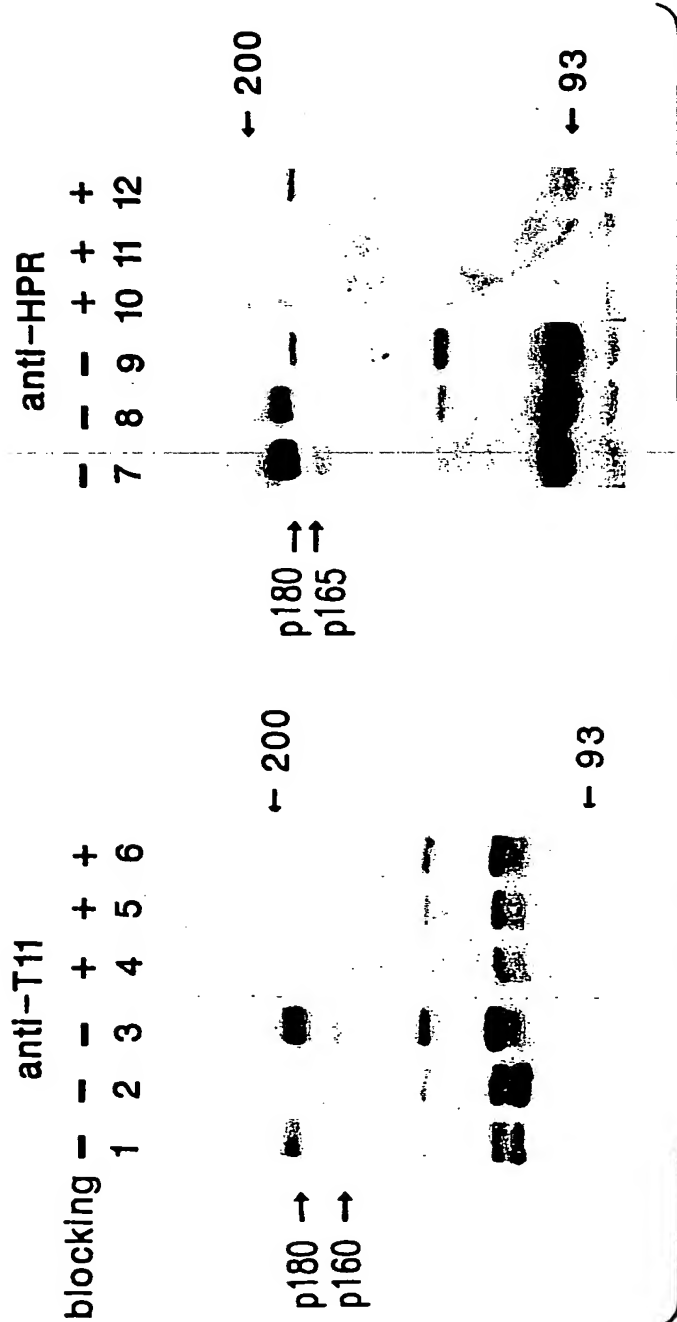


FIG.7A

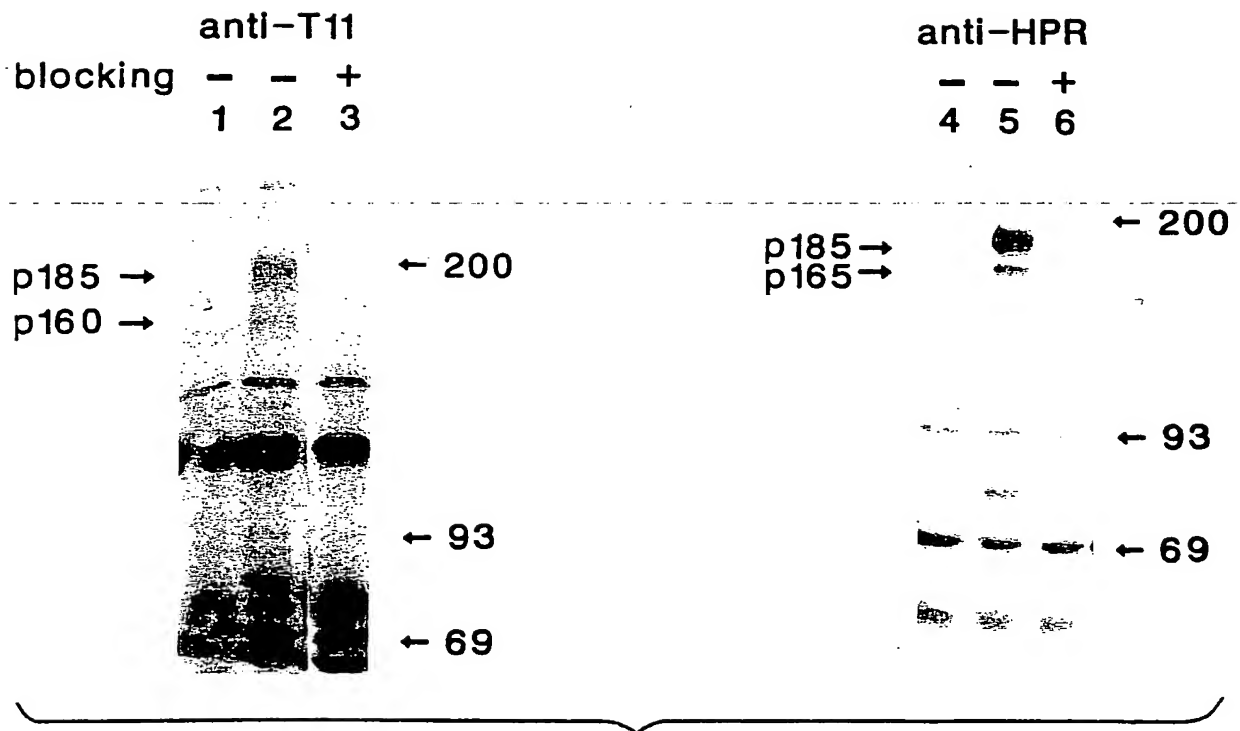


FIG.7B

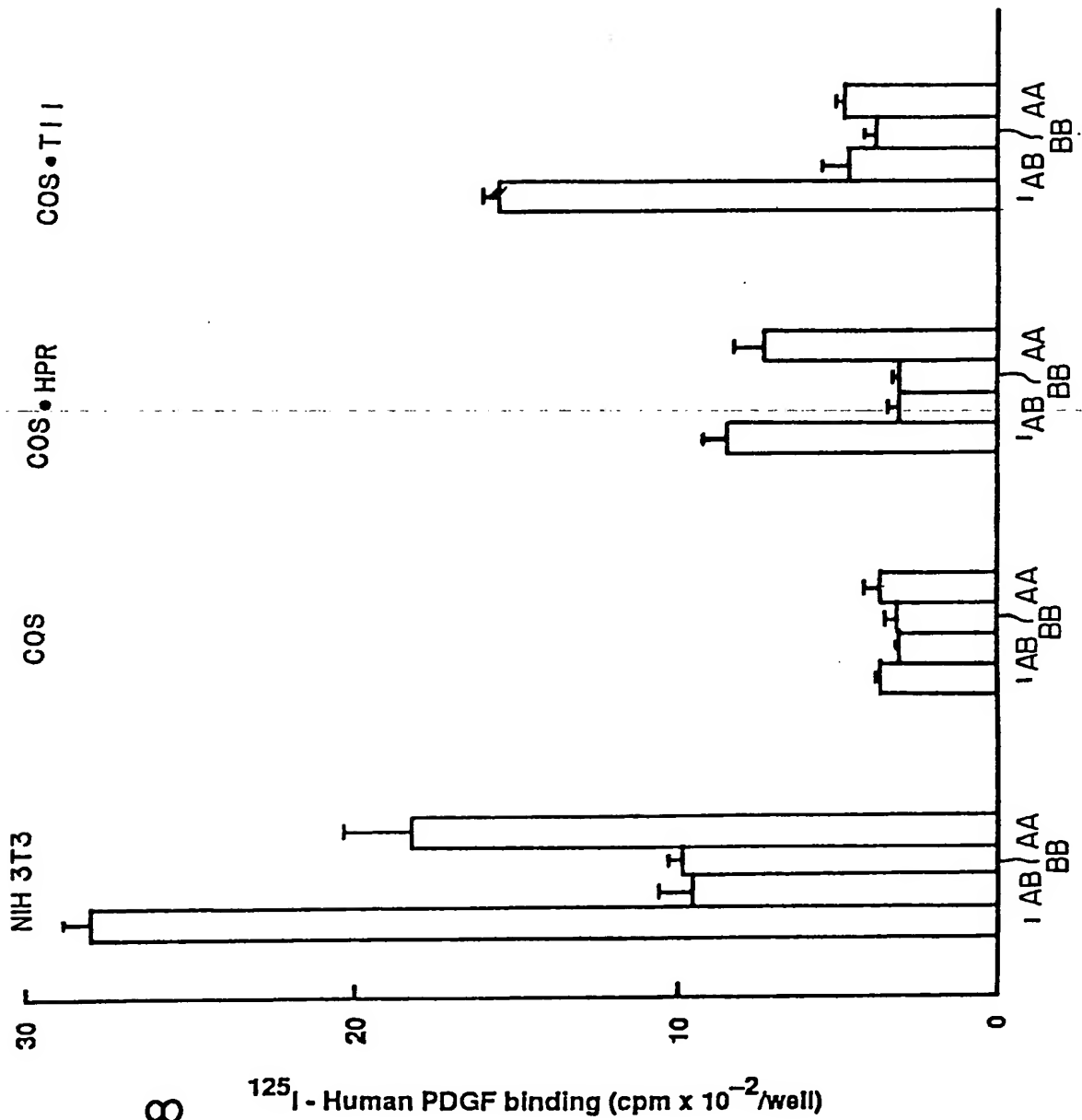


FIG. 8

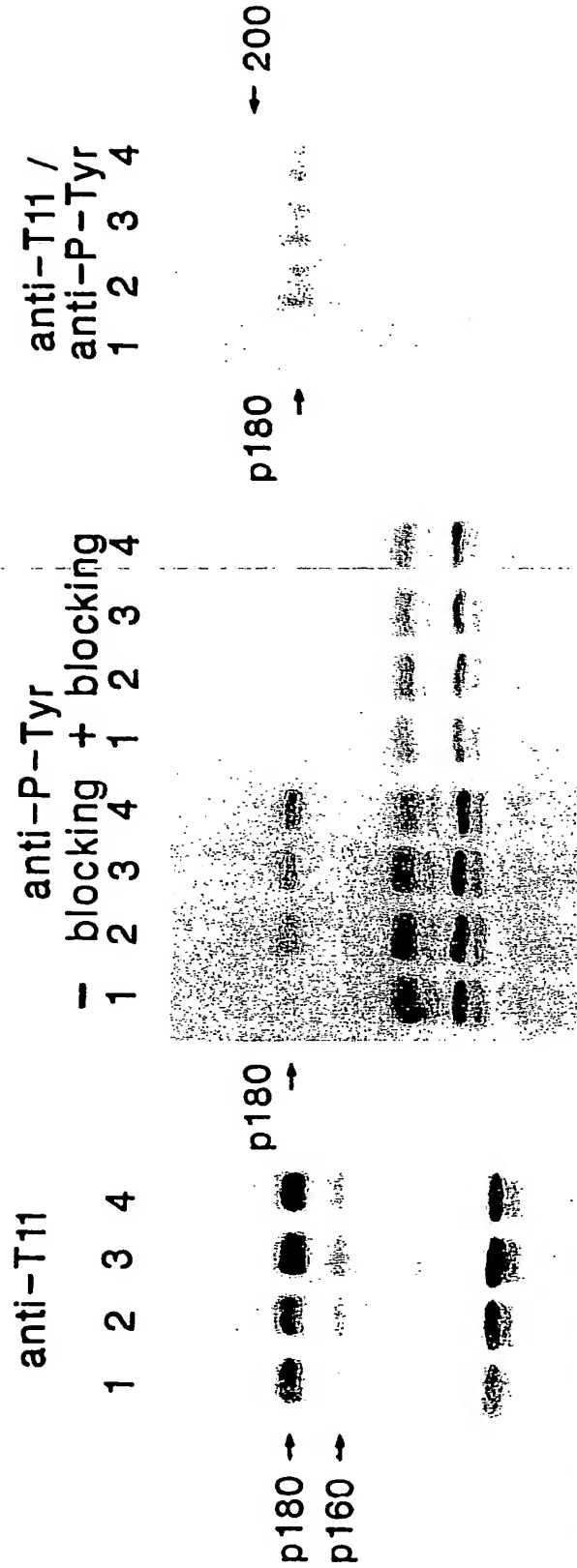


FIG.9A

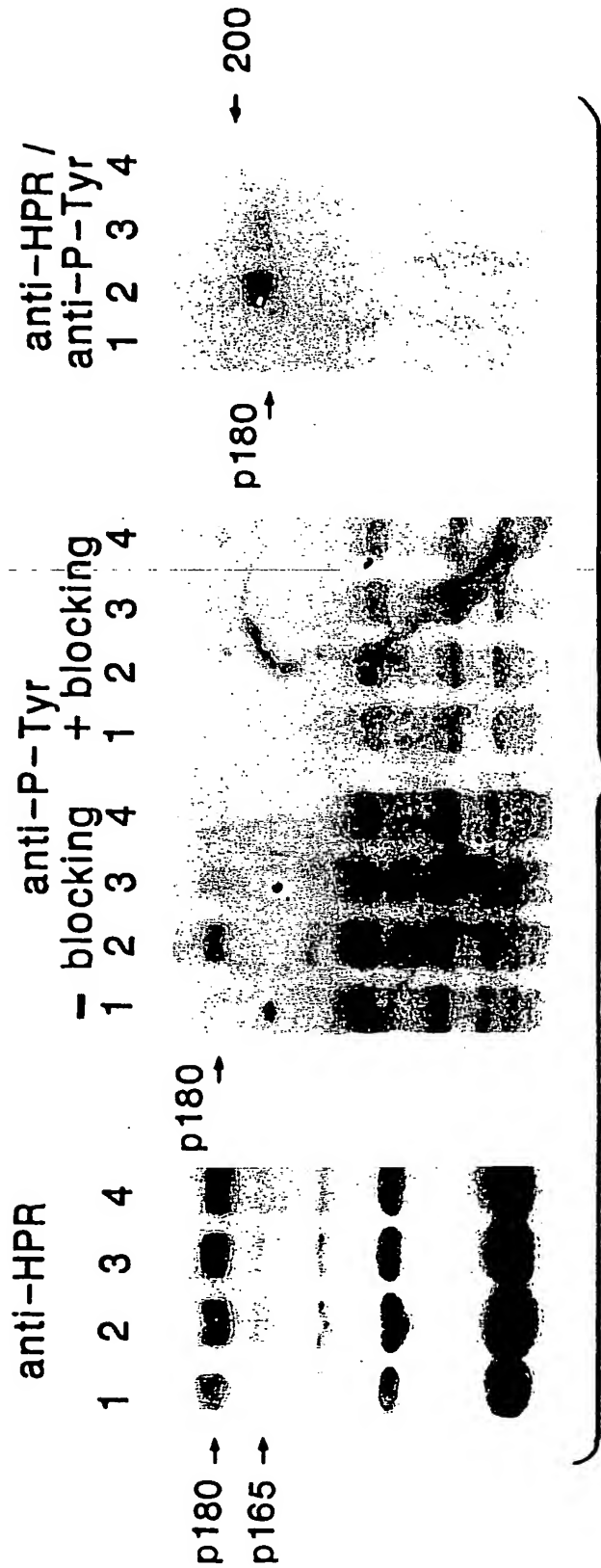


FIG. 9B

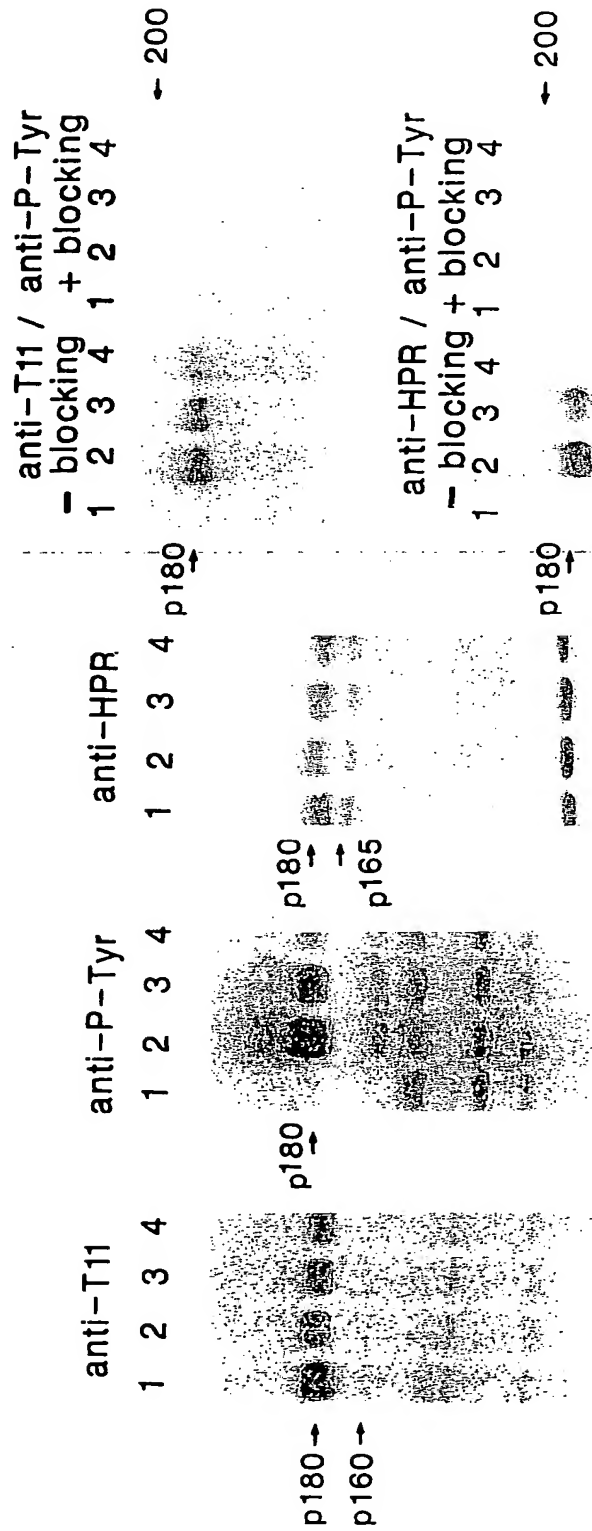
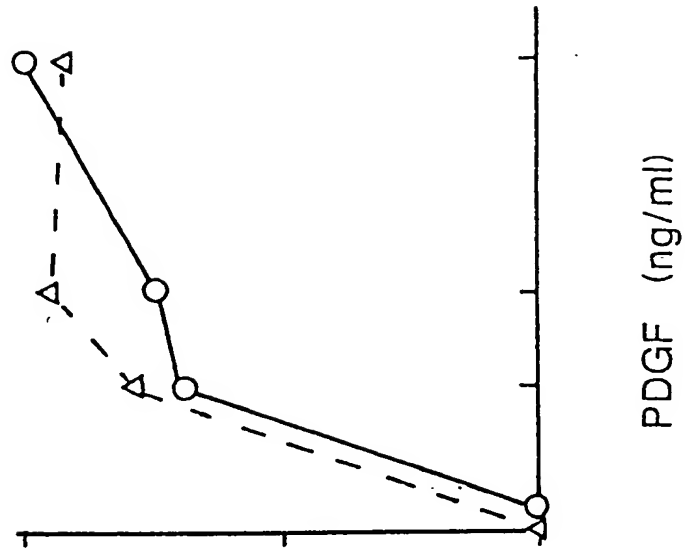


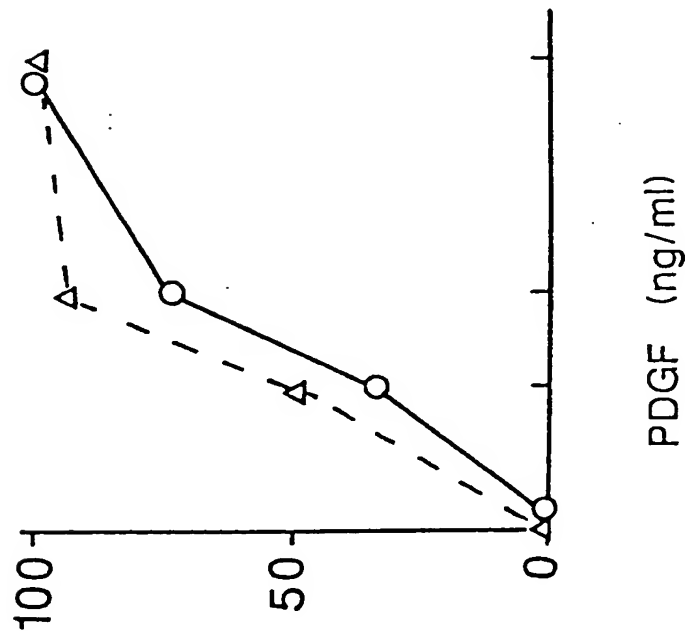
FIG.9C

FIG. 10B



$[^3\text{H}]$ Thymidine Incorporation ($\Delta\text{Max}\%$)

FIG. 10A



$[^3\text{H}]$ Thymidine Incorporation ($\Delta\text{Max}\%$)

FIG. 10D

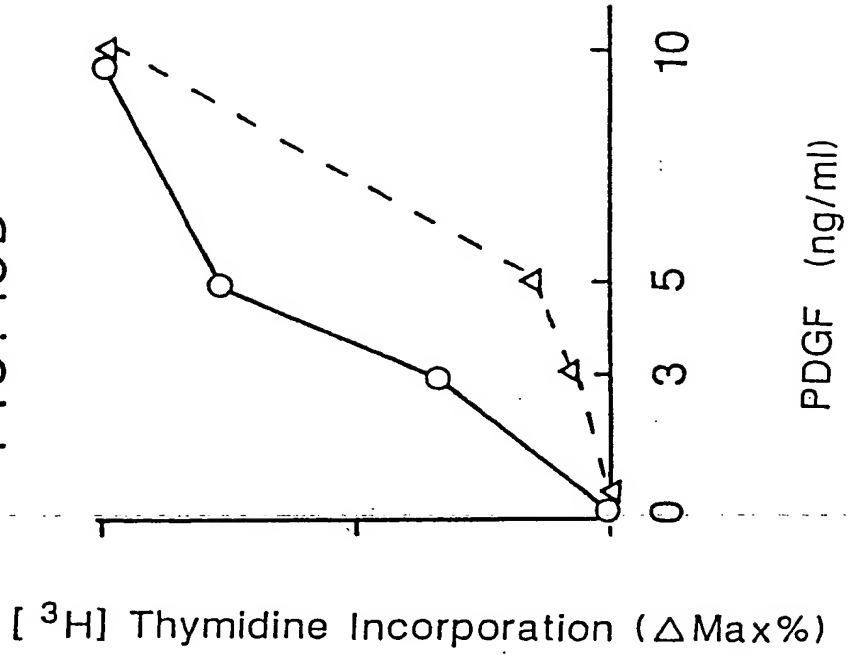
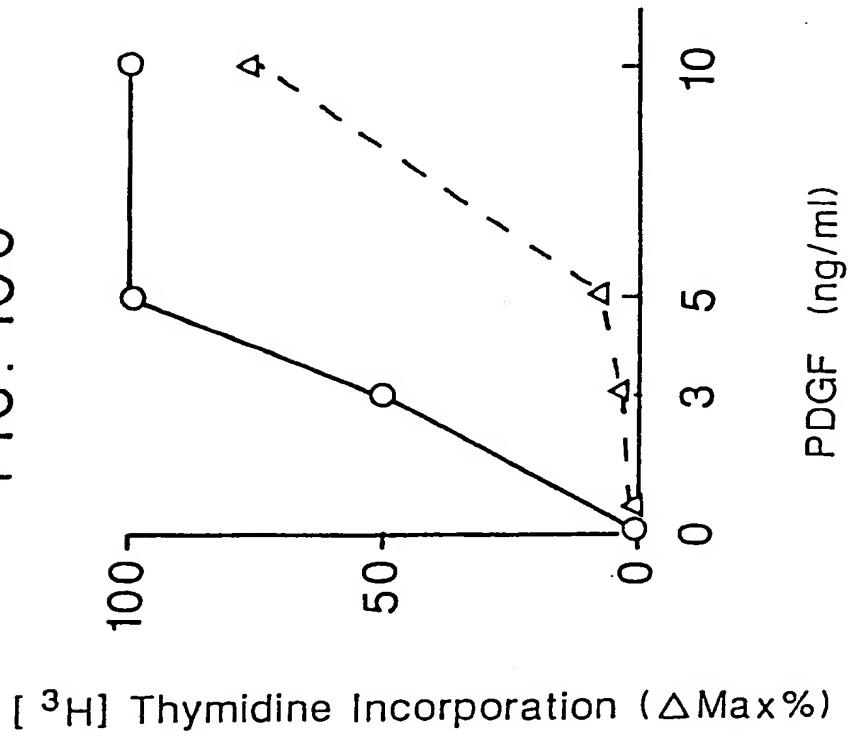


FIG. 10C



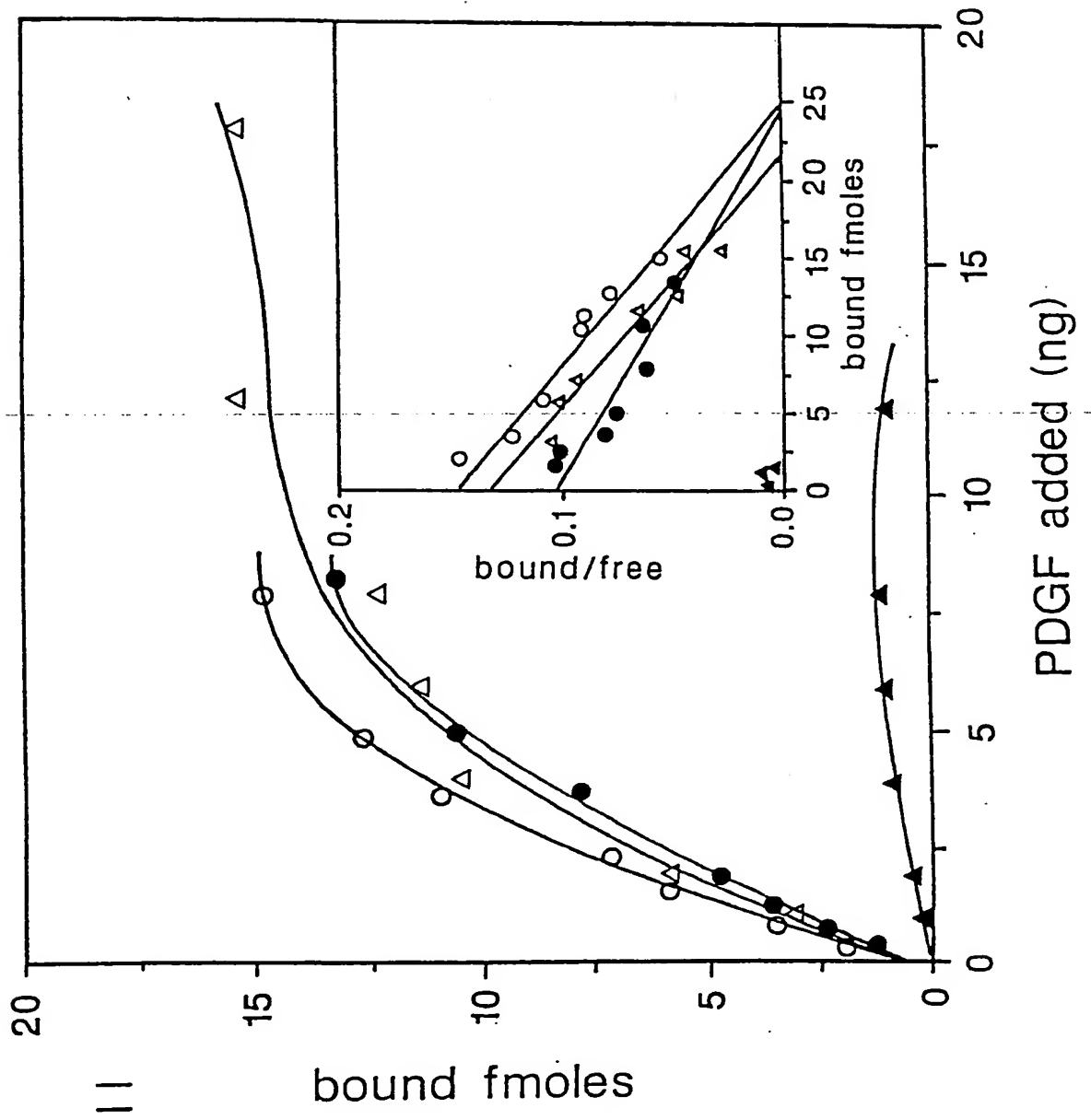


FIG. 11

FIG. 12A

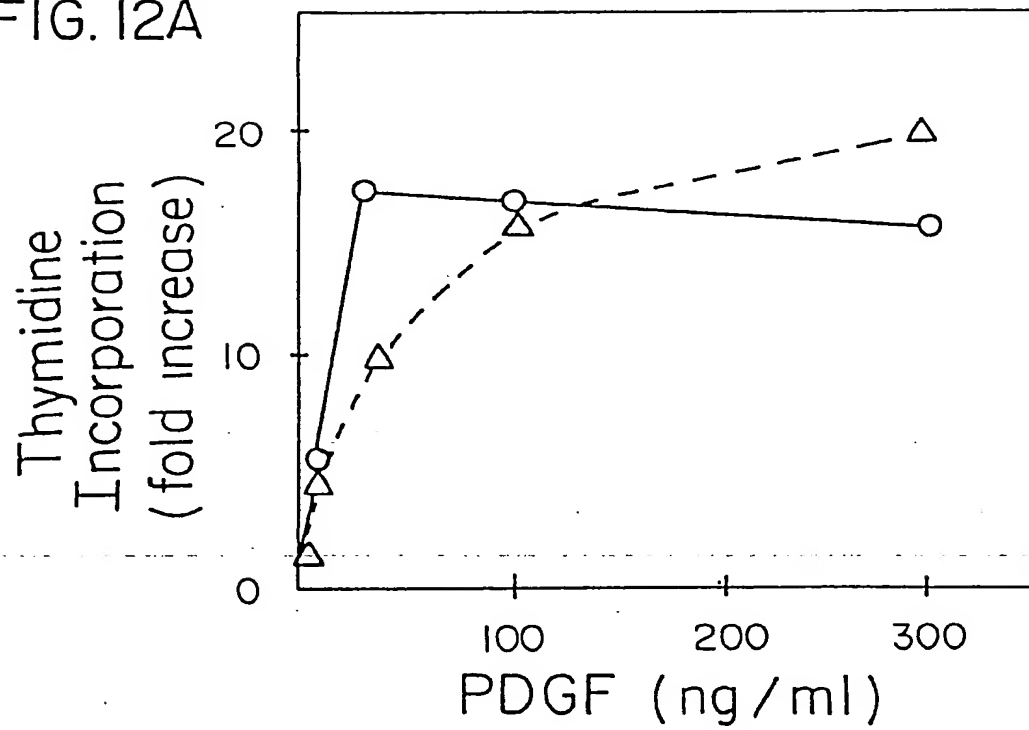


FIG. 12B

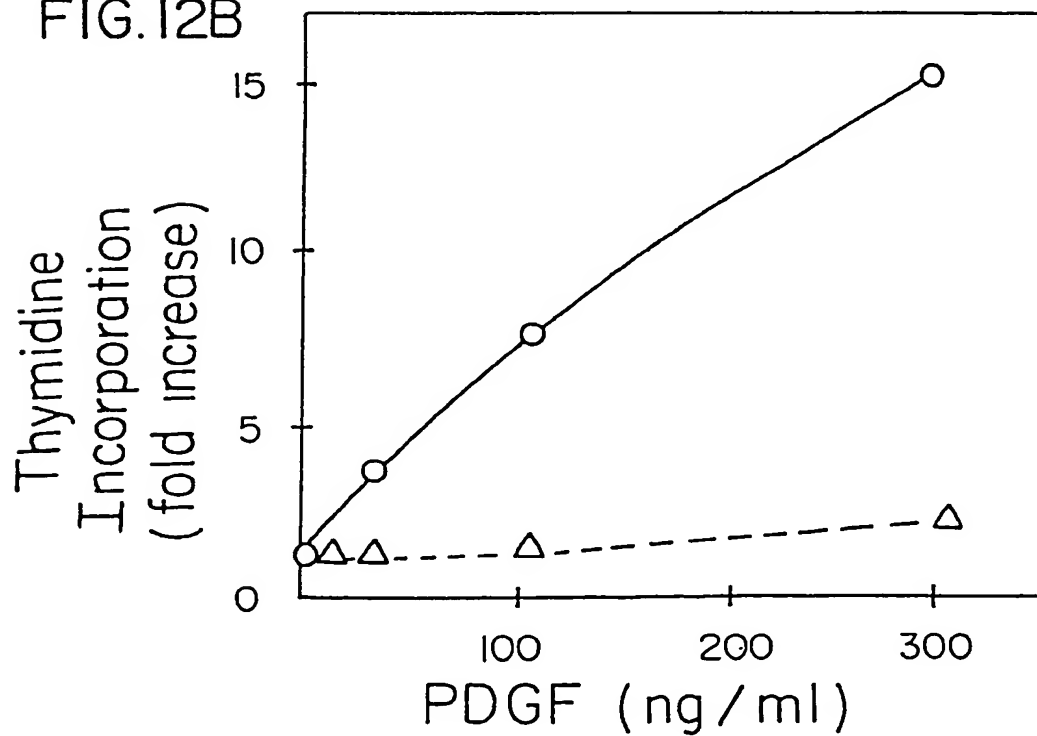


FIG. 13A

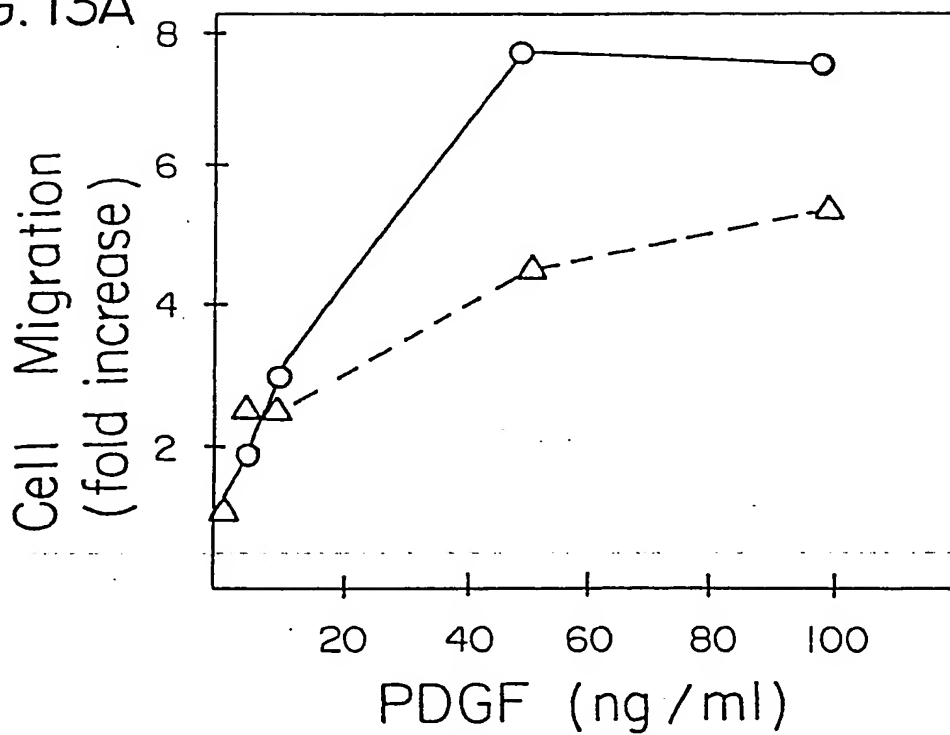


FIG. 13B

